

[illegible][illegible]

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DB 2444 GCGAGCTTGGGAGTACTGCTTGAAGATTAAGTTCCTGCTCTTCTGCGGCTAGCA 2703
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REFERENCE 1 (bases 1 to 1464)
AUTHORS Dwyer, J. P.; Gilliam, J. T. and Maddox, J. R.
TITLE Active polyclonal antibody oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 621434-A 20 03-APP-2001;
FEATURES
Source location/Qualifiers
1..1464 /organism="unknown"
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1b 781 GGAAGCAAAAGATGATGATTCGATACCAAGCTGATACCAAGCTGATC 840
UY 2452 CCAAGCTGATCAGCAAGATGATGATTCGATACCAAGCTGATACCAAG 2511
|||||
1b 841 CCAAGCTGATCAGCAAGATGATGATTCGATACCAAGCTGATACCAAG 900
UY 2512 CCAAGCTGATCAGCAAGATGATGATTCGATACCAAGCTGATACCAAG 2571
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1b 901 CCAAGCTGATCAGCAAGATGATGATTCGATACCAAGCTGATACCAAG 960
UY 2572 CCAAGCTGATCAGCAAGATGATGATTCGATACCAAGCTGATACCAAG 2631
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1b 961 CCAAGCTGATCAGCAAGATGATGATTCGATACCAAGCTGATACCAAG 1020
UY 2632 CCAAGCTGATCAGCAAGATGATGATTCGATACCAAGCTGATACCAAG 2691
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1b 1021 CCAAGCTGATCAGCAAGATGATGATTCGATACCAAGCTGATACCAAG 1080
UY 2692 CCAAGCTGATCAGCAAGATGATGATTCGATACCAAGCTGATACCAAG 2751
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Job time: 13995 sec

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Db	1681	caagcgcacaaagaaatcttgccttatttcttcttcttcttcttcttcttcttcttcttcttcttctt	1740
Uy	1741	cttgcacaaagaaatcttgccttatttcttcttcttcttcttcttcttcttcttcttcttcttctt	1800
Db	1741	cttgcacaaagaaatcttgccttatttcttcttcttcttcttcttcttcttcttcttcttcttctt	1800
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Uy	1981	gcttgcacaaagaaatcttgccttatttcttcttcttcttcttcttcttcttcttcttcttcttctt	2040
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Uy	2581	gcttgcacaaagaaatcttgccttatttcttcttcttcttcttcttcttcttcttcttcttcttctt	2640
Db	2581	gcttgcacaaagaaatcttgccttatttcttcttcttcttcttcttcttcttcttcttcttcttctt	2640

QY	2641	acacgttccatggtcggagaccccgagacgaaatgagtcacacagctcccaagcaatgatacga	2760
DB	2641	acacgttccatggtcggagaccccgagacgaaatgagtcacacagctcccaagcaatgatacga	2700
QY	2701	caaaaatctctgtcttggtggacgaatcccgagagagagcctacggagagagagagagagag	2760
DB	2701	caaaaatctctgtcttggtggacgaatcccgagagagagcctacggagagagagagagagag	2760
QY	2761	gagcgcgcacacagcagctccgaaacacgagtcgagtcgagagagagagagagagagagag	2820
DB	2761	gagcgcgcacacagcagctccgaaacacgagtcgagtcgagagagagagagagagagagag	2820
QY	2841	agcgcgcgcacacagcagctccgaaacacgagtcgagtcgagagagagagagagagagag	2880
DB	2841	agcgcgcgcacacagcagctccgaaacacgagtcgagtcgagagagagagagagagagag	2880
QY	2941	gacatacagatcgatcgatcaacagcagctccgaaacacgagtcgagtcgagagagagag	3000
DB	2941	gacatacagatcgatcgatcaacagcagctccgaaacacgagtcgagtcgagagagagag	3000
QY	3001	tag 3003	
DB	3001	tag 3003	
PPSRF 2			
AAZ60642			
TP	AAZ60642	standard; DNA; 3003 BP.	
XX			
AC	AAZ60642;		
XX			
DT	16-MAY-2000	(first entry)	
XX			
TF	RNA encoding a fusion of aminopolylol amine oxidase/fumonisin esterase		
KW	Aminopolylol amine oxidase; ATRG; mycotoxin degradation; antimicrobial		
KM	Plant fungal invasion; hydrogen peroxide; Fusarium; fungi;		
KX	fumonisin esterase; ss.		
OS	Synthetic.		
OS	Exophiala spinifera.		
XX			
FH	Key	location/Qualifiers	
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FT		esterase fusion"	
FT	sig_peptide	1..72	
FT	/*tag=	b	
FT	/note=	"barley alpha amylase signal sequence"	
FT		73..1575	
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FT		1576..1611	
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XX			
PN	W0200004160-A1.		
XX			
PD	27-JAN-2000.		
XX			
PF	08-JUL-1999;	99WO-0515455.	
XX			

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XX Example 14: Page 115-120; 154pp; English.

XX The present sequence is that of a polynucleotide encoding a
XX fusion protein (see AAY58916) composed of glutathione S-transferase
XX and Escherichia coli lipase (Lipase) joined via a
XX flexible linker to E. coli lipase (see AAY58916), a lipase, but not a
XX lipase, amino polyol amino oxidase of E. coli. The
XX construct was designed for expression in Escherichia coli of a hybrid
XX protein having E. coli and AYO activity. The invention provides AYO
XX polynucleotides (see AAY58916 87) and polypeptides (see AAY58916 85) of
XX E. coli lipase and Escherichia coli lipase. The polynucleotides
XX are used to transform plant cells normally susceptible to Fusarium
XX or other toxin producing fungus infection. Also provided are
XX methods for expressing AYO, optionally as a fusion protein with
XX immunin esterase, in transgenic plants, prokaryotic and non-plant
XX eukaryotic systems. Methods for derivatization of glutathione
XX processing, storage, food crops and in animal feed and rumen
XX microorganisms are also disclosed.

XX Sequence: 3618 BP, 844 A, 525 C, 473 T, 5 other.

XX Query: Match: 97.6%, Score: 2932, DB: 21; Length: 3618;

XX Exact local similarity: 100.00, P-adj: 8e-06;

XX Matched: 2942; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

XX 72 cgtcctactctcaaatgaatgctggagatgctgagtcgagcgaactactgtccggc 131
XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
XX 667 cgtcctactctcaaatgaatgctggagatgctgagtcgagcgaactactgtccggc 746
XX
XX 142 caatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaat 191
XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
XX 747 caatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaat 806
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XX 667 cgtcctactctcaaatgaatgctggagatgctgagtcgagcgaactactgtccggc 926
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XX 412 caatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaat 371
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XX 927 caatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaat 986
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XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
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XX 1447 cgtcctactctcaaatgaatgctggagatgctgagtcgagcgaactactgtccggc 1406
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[illegible][illegible]

[illegible][illegible]

AAZ58400
 ID AAZ58400 standard: cDNA: 2079 bp.
 XX
 AAZ58400:
 XX
 2+ MAY-2090 (first entry)
 XX
 DB DNA encoding 331 truncated amino polypeptide amino oxidase fusion.
 XX
 KW Amino polypeptide oxidase: Amino oxidase: mycelium
 KW Transgenic plant: detoxification, antibiotic, silencing
 KW selectable marker: glutathione S transferase: GST, ss.
 XX
 SS Chimera - Schistosoma japonicum.
 SS Chimera - Escherichia coli.
 XX
 FE Key: 1000/1000/1000/1000
 FE sig_peptide /start - 1
 FE /product: "ast fusion - polypeptide"
 FE /bom: 2076
 FE /mat_peptide /start - B
 FE /product: "K-triAAV"
 FE /musc_feature /start - 1
 FE /start - 1
 FE /note: "extra lysine"
 XX
 FN W200004159-A1.
 XX
 27-JAN-2000.
 XX
 PE 08-JUL-1999: 9960-0815454.
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 PR 15-JUL-1998: 9808-0092636.
 PR 21-MAY-1999: 9908-0145301.
 XX
 PA (FEN-3) F1 NTP H1-BH91 INT INT
 PA (CURA) CURAEN C-8P.
 XX
 PI Towick JP, Gilliam JL, Mallick JR
 XX
 WP1: 2008-18247/16,
 DR P-PSDB: AAY58911.
 XX
 PI New isolated polypeptides, polypeptides useful for detecting and
 PI degrading tumours or structurally related mycoplasma in processed
 PI grain or in silage.
 XX
 PE Example 2: From WO/92/15449, Example 2
 XX
 SS The present sequence is that of a polypeptide encoding a
 SS GST-K-triAAV fusion protein composed of glutathione S transferase
 SS and K-triAAV. It is composed of two fused genes: amino polypeptide
 SS oxidase (see also AAZ58400) of Escherichia coli. The construct
 SS was designed for expression of K-triAAV in Escherichia coli.
 SS K-triAAV is capable of degrading fumonisin and related mycotoxins.
 SS The inventors further discovered that K-triAAV (27) and
 SS polypeptides (see AAY58911) of E. coli and Rhizoglyphus
 SS atrovirescens. The polypeptides are used to transform plant cells
 SS normally susceptible to fumonisin or other toxin by inducing fumonisin
 SS infection. Also provided are methods for expressing K-triAAV in
 SS transgenic plants, prokaryotic and non-plant eukaryotic systems.
 SS Methods for detoxification of grain, grain processing, silage, food
 SS crops and in animal feed and human microorganisms are also disclosed.
 SS AAVO polypeptide can also be used as a selectable marker.
 XX
 XX Sequence 2079 bp: 517 A, 193 C, 517 G, 595 T, 8 other.

Query Match: 46.4%, Score 1395, Db Z1, Length 2076;
 Best Local Similarity: 100.0%, Seed No. 0;
 Matches 1394: Consensitive 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 687 cgaagaaacgcttgagagcgtgattggtggcgctgattgaacgctttggaacacac 746
 QY 1671 agcgaagatccagagcgagcgtgattggtggcgctgattgaacgctttggaacacac 1730
 DB 747 agcgaagatccagagcgagcgtgattggtggcgctgattgaacgctttggaacacac 806
 QY 1731 ggaagaaacgcttgagagcgtgattggtggcgctgattgaacgctttggaacacac 1790
 DB 807 ggaagaaacgcttgagagcgtgattggtggcgctgattgaacgctttggaacacac 866
 QY 1791 tgggtgagcgaatgagagcgaacgaacgaacgaacgaacgaacgaacgaacgaacgaac 1850
 DB 867 tgggtgagcgaatgagagcgaacgaacgaacgaacgaacgaacgaacgaacgaacgaac 926
 QY 1851 tgggtgagcgaatgagagcgaacgaacgaacgaacgaacgaacgaacgaacgaacgaac 1910
 DB 927 ggaagaaacgcttgagagcgtgattggtggcgctgattgaacgctttggaacacac 986
 QY 1911 cgaagaaacgcttgagagcgtgattggtggcgctgattgaacgctttggaacacac 1970
 DB 987 cgaagaaacgcttgagagcgtgattggtggcgctgattgaacgctttggaacacac 1046
 QY 1971 actgcctcctccttgggtgctgattggtgagagcgaacgaacgaacgaacgaacgaacgaac 2030
 DB 1047 actgcctcctccttgggtgctgattggtgagagcgaacgaacgaacgaacgaacgaacgaac 1106
 QY 2031 cctcgaagaaacgcttgagagcgtgattggtggcgctgattgaacgctttggaacacac 2090
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 QY 2091 ctggcctcctccttgggtgctgattggtgagagcgaacgaacgaacgaacgaacgaacgaac 2150
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 QY 2211 cctcgaagaaacgcttgagagcgtgattggtggcgctgattgaacgctttggaacacac 2270
 DB 1287 cctcgaagaaacgcttgagagcgtgattggtggcgctgattgaacgctttggaacacac 1346
 QY 2271 gatttgcgaagcgttgcgaagcgttgcgaagcgttgcgaagcgttgcgaagcgttgcgaagcgtt 2330
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 QY 2331 cctcgaagaaacgcttgagagcgtgattggtggcgctgattgaacgctttggaacacac 2390
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 DB 1707 atggtcgaatcgttgcgaagcgttgcgaagcgttgcgaagcgttgcgaagcgttgcgaagcgttgcgaagcgtt 1766
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Sequence ID Application US/2017/02159A
Parent No. 6211434
GENERAL INFORMATION
APPLICANT: DIVIACK, Jonathan P.
APPLICANT: Gilliam, Jacob L.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Active Polymers and Related Polypeptides and Methods of Use
FIELD OF INVENTION: Polymers and Related Polypeptides and Methods of Use
FILE REFERENCE: 1124
CURRENT APPLICATION NUMBER: US/2017/02159A
CURRENT FILING DATE: 10-06-2017
EARLIER APPLICATION NUMBER: US/2017/02159A
EARLIER FILING DATE: 10-06-2017
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 10-06-2017
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 3.0
SEQ ID NO: 16
LENGTH: 1673
TYPE: DNA
ORGANISM: Escherichia coli
FEATURES
NAME: CDS
LOCATION: (1)...(267)
OTHER INFORMATION: gene alpha coding part of secreted signal
NAME: CDS
LOCATION: (1)...(1662)
US-00-000000-1

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OTHER INFORMATION: K: LysA, codon usage: 0.001100, 0.003667, 0.00
OTHER INFORMATION: codon, for bacterial expression.
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2376)
NAME/KEY: misc_feature
LOCATION: (1)..(687)
OTHER INFORMATION: get_feature polypeptide
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OTHER INFORMATION: K: LysA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1217)..(1733)
OTHER INFORMATION: Extra lysine
US-09-457, 159, 18

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[illegible][illegible]

WAS CONSTITUTED by Dr. Claudio Schneider (LNUB-Arge-
 26 June 1948, T-1050, 1411)
 BASE COLONY
 120 g 116 g 158 g 73 g
 GELATIN

Best Local Similarity 100.0%; Pred. No. 19;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 1291 tttaaaatcttaaaattttc 1281
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 34 427 tttaaaatcttaaaattttc 407

Search completed: August 16, 2002, 08:56:27
 Run Time: 10:11 Sec

MMOT: US-09-658-8350 25 to: 06/16/11 * out_format: pdf

About: Results were produced by the vendor's software, version 4.0.
 Copyright (c) 1993-2000 CompuGen Ltd.

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Query length: 1800
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DEFINITION sequence 24 from patent US 6211434.
ACCESSION AB145459

VERSIN
A0144458.1 51:1510325

SOURCE:
ORGANISM
UNKNOWN.

UNCLASSIFIED;
1 (Pages 1 to 3003)

TITLE Amino polyol amino oxidase polynucleotide

JOURNAL Patent: US 6,211,434 A 24 03 APR-2001

source 1. .3003

BASH: COUNT	690 a	840 c	819 q
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quality: 5304 00

Percent similarity: 100,000 Percent

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3.4 $\{v_1, v_2, v_3, v_4\} \subseteq V(G)$. Then $\{v_1, v_2, v_3, v_4\} \subseteq V(G)$.

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51 GluPheLeuCl⁻Val¹ProPheAla¹²IleSer¹³

151 5A5161455510014465555100

67 Other Approval Provisions

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84  FOA1ACYSFRC:INCINPhcASNTYrPrO1
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[illegible]

101 MELANOLIPIDIN HYDROLYSIS

301 A16602160110AA1A:ACC0000000001CA:

THE UNIVERSITY OF CHICAGO

1. **Introduction**
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 217. **Figure 209**

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TITLE	Accession	Gene	Enzyme	Substrate	Product	EC	Source	Location	Qualifiers
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51	AF014548	51	51	51</					

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443  dPhetIyThrTYR.....ProVal 447
1901 TTTTGGAGTGTTCAGACTGAGCTGGTGTGTTCATTGGCGCCG 1950
448  AlAserAlaThrAlaLeuGluAlaGlnThrSerLysTyrMetGluGlyAl 464
1951 GAGAGGAGCGAGCGCGCGAGCGAGCTGGTGTGTTCAGACTGAGCTGGC 2000
464  dTPAlaAlaPheAlaLysAsn.....PrometAsnG 475
2001 GTGGGTCGGTGTGTTCAGAGATGTTCAGCGCGAGCGCTGGTGTTCCT 2050
475  LyrProValIlePheSerGluValIleProAsnValAlaAlaLeuLysSerProGly 491
2051 GCGGTGGCTATTCTTACGGGCAACTGACCAATTCAGTGGTGGCAGGCT 2100
492  LysAlaIleLeuIleValaLysPheLysProAlaThrIleAspGluArgGlyAl 508
2101 GCGGAGT.....GCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2144
508  dLeuTYrThrArgTYrTYrThrGluLeuGlyThrIleValaPheArgPheP 525
2145 G.....GATGGCGGTAAAGGCGG 2161
525  hcdIyGlyIleLysSerGlyGlyGlySerGlyGlyLysSerLysAspAsnVal 541
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542  AlaAsnValValaValaGlyAlaGlyLeuSerGlyLeuGluThrAlaArg 558
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2262 CAAAGTCCAGAGCGCGCGCGGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 2311
575  TAYValGlyGlyGlySerThrLeuSerValGlnSerGlyProGlyArgThr 591
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592  IleAspAspLeuGlyAlaAlaArgPheAsnAspSerAsnGlnSerGlyAla 608
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625  hcdIyAsnSerIleHISGlnAlaGlnAspGlyThrPheThrThrAlaPro 641
2462 GTGAAATTCATTCATCAACACCAAGAGGAGGAGGAGGAGGAGGAGGAG 2511
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2512 TATGTGACCTCTTCTGAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 2561
658  dLeuTYrValIlePheSerGluLeuIleGluGlnIleSerLeuGluAspLeu 675
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675  LysAlaSerProGlnAlaLysArgLeuAspSerValSerPheAlaHisTYR 691
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692  CysGlnIleLysIleLeuAsnLeuProAlaValaLeuGlyValaAlaAsnGlu 708
2662 TGTGAGAAAGAACTAAGCTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2711
708  PheArgValaAlaLeuLeuGlyValaGlnAlaHisIleIleSerMetLeuPhe 725
2712 CAAAGAGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2762
725  dThrAspTYrIleLysSerAlaThrGlyLysSerAsnGlnPheSerAsp 741

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742  LysLysAspGlyGlyGluPheArgLysGlySerGlyMetGluGlnIle 758
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758  CCGSHISAlaMetSerLysGlnGluValaIleGluGluValaHisIleGluSer 775
2862 TGTGATGTCATGTCAAGAGAACTGTGTTCAGGCTGATGAGGCTGAGCA 2911
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2912 CCGGCTGGTGGCAATTCAGAGGTGCAATGGGTGTATCTATCTATCTATCT 2961
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2962 GCGTGGGAGCGCGGTGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 811
808  PThrLeuTYrThrPheThrLeuThrPheSerProProGluProAlaGluGlyG 825
3012 AAGCTTGATGCACTGCAATTTTCAGTACGCTGTTTGGTGGTGGTGGTGG 8361
825  LysAlaLeuAlaGlnAsnSerIleLeuGlyTYrTYrSerTYrLysValaPhe 841
3062 AAGATTGGCGGAAATTCATTCCTGGGCTACTATAGCAGATGAGTCTTC 8111
842  ValIlePheArgLysProPheThrArgGlnGlnGlyPheSerGlyValaLeu 858
3112 GTATGCGCAAGCGGTGGTGGGCAACAGAGCGCTTCGAGGAGGAGGAGGAG 861
858  LysSerSerLysAspProIleSerProValaArgAspIleSerIleAspVala 875
3162 ATCGAGCTGTGACCGCATTCATTGTCAGAAATATCAGATTCAGCTGGC 8211
875  SPArgGlnThrSerIlePheThrSerMetValaGlyAspProGlyArgThr 891
3212 ATCGACAAATGTCATTATATGTTTATGCTTGGAGAGGAGGAGGAGGAG 8261
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3262 TGGTGGCGAGCTGTCAAGCTAGCTATACCAAAAGCTGTGGGAGGAGGAG 8311
908  dArgAlaAlaArgGluAsnAlaGlyAlaGluValaProGluProAlaAsnV 925
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seq_documentation_block: 3591 bp CNA linear Feb 08 AUG 2001
Locus: AK145488
DEFINITION Sequence 30 from patient US 6211445.
ACCESSION AK145488

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568 LeuValIleuGluAlaMetAspArgValGlyIleThrIlePheValGlu 584
592 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 591
584 AsnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 601
592 ArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 601
601 SerAspSerAsnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 617
602 AlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 651
618 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 634
652 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 701
634 ProIleThrIleThrIleProIleThrIleProIleThrIleProIle 651
702 GlnIleAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 751
651 dAlaSerAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 667
752 ThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 801
658 GlnIleSerIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 684
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684 ProValIleProIleAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 701
852 GlnIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 901
701 dAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 717
902 ThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 951
718 HisGlnIleSerMetIleProIleGlnGlnGlnGlnGlnGlnGlnGln 744
952 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1001
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751 ThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 767
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768 ProIleSerValIleIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 784
1102 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1151
784 dSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 801
1152 ThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1201
801 ThrValValValSerGlnProIleThrIleProIleThrIleThrIle 817
1202 ArgIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1251
818 ProIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1271
1252 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1301
834 ThrIleThrIleThrIleThrIleThrIleThrIleThrIleThrIle 851
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851 ThrIleThrIleThrIleThrIleThrIleThrIleThrIleThrIle 867
1352 ThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1401

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868 ArgAspThrSerIleAspValAspArgGlnThrSerIleThrIleThrIle 884
1402 AGAGATACCAATATGAGCTGATATACAAATGATATACCTGTTTCAAT 1451
884 ValGlnIleProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 901
1452 GGTGAGACACCGGATGAGAGTGGTGTCCAACTACCTAAAGTAAAGTAC 1501
901 ThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 917
1502 AAAATGCTGCTGAGACCAACCTCCGCGTACGCTAACCAACCGCGGAGCC 1551
918 GlnValIleProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 934
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934 nTyrPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 951
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951 ThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 967
1652 CACTGCGCTTCCGCGCTGAGAACCGGCTGCAAGAGTATGATTCATGGA 1701
968 ThrGlnIleProIleValIleThrGlnGlnGlnGlnGlnGlnGlnGln 984
1702 ACCAGAGCGCTTTCAGTTTGCAGAGCTATATGAGAGCGCGCTATACCAT 1751
984 ThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1000
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seq_name: gb_pat:AR145462
seq_documentation_block:
LOCUS AR145462 2490 bp DNA linear MAY 08 2001
DEFINITION Sequence 32 from patent US 6211434.
ACCESSION AR145462
VERSION AR145462.1 GI:15107329
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 2490)
AUTHORS Duvalick, J.P., Gilliam, J.T. and Maddox, J.R.
TITLE Anticancer agent and methods of use
JOURNAL Patent: US 6211434-A 32 03-APR-2001;
FEATURES
location/Qualifiers
1..2490
BASE COUNT 625 a 623 c 653 g 589 t
ORIGIN
alignment_scores:
Quality: 2490.00 Length: 651
Ratio: 4.369 Gaps: 8
Percent Similarity: 84.025 Percent Identity: 75.883

alignment_block:
US 09 658 835c 25 A Ar145462 ..
At:gb seq 1/1 to AR145462 from 1 to 2490

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638 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 707
731 ThrIleThrIleThrIleThrIleThrIleThrIleThrIleThrIle 746
708 c ATCAATGCTTAAAGGATGATGATGATGATGATGATGATGATGATGAT 754

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386  LALALALLeuThrGluValArgPheLeuIleProSerAlaIleValAla 402
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756  GTCATGGTCAGACGAGCGAGGTATGTGCAATAGCTGACAGATTGCA 804
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408  GlnAAspGlnAspGlnAspGlnAspGlnAspGlnAspGlnAspGln 419
      ::::: ::::: ::::: ::::: :::::
804  CAATGAGGCTGAGGCTGAGGAGGAGGCTGAGGAGGAGGAGGAGGAG 854
      ::::: ::::: ::::: ::::: :::::
419  dHhPheGlnAsnLeuGln.....LeuPheProGlySerGlnValIT 433
      ::::: ::::: ::::: ::::: :::::
859  AGGATTCGATGCAATGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCA 904
      ::::: ::::: ::::: ::::: :::::
433  LeuIleSerLeuGlnValGlyMetValPheGlyThrProValAlaSer 449
      ::::: ::::: ::::: ::::: :::::
905  ATGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 954
      ::::: ::::: ::::: ::::: :::::
450  ALAAlaAlaGlnGlnAlaGlnThrSerLeuGlnGlnGlnValAlaP 466
      ::::: ::::: ::::: ::::: :::::
959  GTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 983
      ::::: ::::: ::::: ::::: :::::
466  dAlaPheGlnAlaGlnAspProMetAsnGlyProGlyTyrPheGlnValPro 483
      ::::: ::::: ::::: ::::: :::::
984  TACCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026
      ::::: ::::: ::::: ::::: :::::
484  sHValAlaAlaLeuGlySerProGlyLysAlaIleLeuValAlaSer 499
      ::::: ::::: ::::: ::::: :::::
1027  ..GCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1074
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506  ProAlaThrIleAspGlnAspGlnAlaLeuGlyThrArgTyrThrThr 516
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1074  ..... 1074
516  dLeuGlyThrIleAlaPheArgThrPheGlyGlyLysSerGlyLys 533
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1075  .....GCGCTGGTGGCG 1086
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533  eGlyGlyGlySerLysAspAsnValAlaAspValValValGlyAla 549
      ::::: ::::: ::::: ::::: :::::
1087  ..GAGTAAACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1134
      ::::: ::::: ::::: ::::: :::::
550  GLeuSerGlyLeuGlnThrAlaArgLysValGlnAlaGlnLeuSer 566
      ::::: ::::: ::::: ::::: :::::
1135  GAGCTTGAAGGCTTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1184
      ::::: ::::: ::::: ::::: :::::
566  rTyIleValIleuGlnAlaMetAspArgValGlyGlyLysThrLeuSer 583
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1185  GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1234
      ::::: ::::: ::::: ::::: :::::
583  dGlnGlnSerGlyProGlyArgThrThrIleAsnAspLeuGlyAlaAla 599
      ::::: ::::: ::::: ::::: :::::
1235  TACATTCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1284
      ::::: ::::: ::::: ::::: :::::
600  LLeuAspSerLeuAsnGlnSerGlnValSerArgLeuPheGlnArgPhe 616
      ::::: ::::: ::::: ::::: :::::
1285  ATCTGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1334
      ::::: ::::: ::::: ::::: :::::
616  sLeuThrGlyGlyLeuGlnArgThrThrGlyAsnSerIleHisGlnAla 633
      ::::: ::::: ::::: ::::: :::::
1335  TTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1384
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633  LAspGlyThrThrThrAlaArgTyrGlyLysSerLeuLeuSerGln 649
      ::::: ::::: ::::: ::::: :::::
1385  AACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1434
      ::::: ::::: ::::: ::::: :::::
650  GLeuValAlaSerAlaAlaGlnLeuLeuProValTyrSerGlnLeu 666
      ::::: ::::: ::::: ::::: :::::
1435  GAGTTTGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1484
      ::::: ::::: ::::: ::::: :::::
666  eGlnGlnHisSerLeuThrAspLeuGlyAlaSerProGlnAlaGlyArg 683
      ::::: ::::: ::::: ::::: :::::
1485  TCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1534
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683  eAspSerValSerPheAlaHisTyrGlnGlnLeuGlnLeuSerGln 699
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1535  TCGAGGCTGAGGCTTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1584
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708  AlValIleuGlyValAlaAsnGlnIleThrArgAlaLeuLeuGlyVal 716
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1585  GCTGTTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1634
      ::::: ::::: ::::: ::::: :::::
716  dAlaHisThrIleSerMetLeuPheLeuThrAspPheIleLeuSerAla 733
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1635  AGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1684
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733  hGlyLeuSerAsnIlePheSerAspGlyLysAspGlyLysValTyrMet 749
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1685  GCGCTGCTGAGTAATTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1734
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750  ArgCysTyrSerGlyMetGlnSerIleGlySerAlaIleSerLeuSer 766
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766  sValProGlySerValIleLeuAsnThrProValAlaGlnIleGlnHis 783
      ::::: ::::: ::::: ::::: :::::
1785  TCTTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1834
      ::::: ::::: ::::: ::::: :::::
783  eAlaSerGlyCysThrValArgSerAlaSerGlyValIlePheArgSer 799
      ::::: ::::: ::::: ::::: :::::
1835  CGGATCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1884
      ::::: ::::: ::::: ::::: :::::
800  LysLysValIleValSerLeuPheThrThrProGlyThrProThrPhe 816
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1885  AAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1934
      ::::: ::::: ::::: ::::: :::::
816  eSerProProLeuProAlaGlnLysGlnAlaLeuAlaGlnAsnSerIle 833
      ::::: ::::: ::::: ::::: :::::
1935  TTCAGGAGGCTTTGCGGCGGAGAAACAGGAGGAGGAGGAGGAGGAGG 1984
      ::::: ::::: ::::: ::::: :::::
833  eGlyTyrTyrSerLysLeuValIleValThrLeuLeuLeuThrProG 849
      ::::: ::::: ::::: ::::: :::::
1985  TGGATATATATATATATATATATATATATATATATATATATATAT 2034
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850  GlnGlnLysPheSerGlyValIleuGlnSerCysAspProIleSerPh 866
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2035  GAAACAAGGCTTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2084
      ::::: ::::: ::::: ::::: :::::
866  eAlaArgAspThrSerIleAspValAspArgGlnThrSerIleThrLys 883
      ::::: ::::: ::::: ::::: :::::
2085  TGGCAGAGATTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2134
      ::::: ::::: ::::: ::::: :::::
883  hMetValGlyAspProGlyValGlySerProGlnGlnSerLysGlnVal 899
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2135  TCATGCTGAGAGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2184
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900  ArgGlnLysSerValTyrAspGlnLeuValAlaIleTyrGlnAsnAla 916
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2185  GAGTAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2234
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916  ValGlnValProGlnProValAsnValLeuGlnIleLeuThrProSerLys 933
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2235  GCTTCAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2284
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933  GlnGlyThrGlnGlyValAlaProSerAlaValTyrGlnLysAspLeu 949
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2285  AGCAGTATTTCCAGGAGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2334
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950  LThrLeuGlySerAlaLeuArgThrProLeuLysSerValHisPheVa 966
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2335  ATCCAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2384
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966  GLeuThrGlnThrSerLeuValTyrLeuLeuLeuLeuLeuLeuLeu 983
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2385  TCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2434
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983  eSerGlyLeuArgGlyValAlaGlnValAlaLeuSerLeuValProAla 999
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767 ValProGlySerValHisLeuAsnThrProValAlaGlnIleGluGlnSer 783
|||||
1375 GTTCAAGGCTTCAAGAGCTTAAAGAGGAGGAGGCTGCAATTCAGACGTC 1424
784 LAlaSerGlyCysIleValIleAspAlaSerGlyValAlaAlaPheArgSerL 800
|||||
1425 GGCATCCGCGCTGTAAGTACGATTCGCTGAGCGCGCTGCTCCAGAGTA 1474
800 ySLysValValValSerLeuProThrIleLeuTyrProThrLeuThrPhe 816
|||||
1475 AAAAGTGGTGGTTGGTTCACCGAAAGCTTCACTTCACTTCACTTCACTT 1524
817 SerProThrLeuProAlaGlnIleGlyHisAlaGluAlaHisSerIleLeu 833
|||||
1525 TTAACAACCTCTTCCGCGAAGAAATAGATATGGTCAAAATTTATCTCT 1574
834 ySLYFSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 950
|||||
1575 GAGCTACATACAAATACGCTTCGCTATCGCAAGAGGAGGAGGAGGAGG 1624
850 IuGluGlyThrSerThrValLeuGluGluSerCysAspProIleSerPhe 866
|||||
1625 AACAAAGTCTCTGAGGCTCTTCAATCAAGCTGCAAGGCAATTCATCTT 1674
867 AlaAlaAspThrSerIleAspValAspArgGlnThrPheSerIleThrCysPh 884
|||||
1675 GGTAAAGATATGATATGATGATGATGATGATGATGATGATGATGATG 1724
884 QMerValIleAspProGlyArgLysTrpSerGluHisGlySerIleValA 900
|||||
1725 CATGGTGGAGAGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1774
900 PGLIYSSSTVALIIPSPGIGLQWATGALALGTYGTLQASGATAGLY 916
|||||
1775 GACAAAGATTCCTCGGGAGCAACTCCGCGAGGCTACGACAAATCCCGGG 1824
917 AlacIlnValProGlnProAlaAsnValLeuGlnIleGluIlePheLysG 933
|||||
1825 GCCCAAGTCCTAAGTCCGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1874
933 nGLuIlePheGlnIleGlyAlaProSerAlaValIleTyrIleLeuAsnAspLeu 950
|||||
1875 GCAAGATTTCCAGAGAGGCTCCGAGGAGGAGGCTATAGGAGCTGAAAGATCTCA 1924
950 LcThrLeuIleSerAlaLeuArgGlnThrProMetLysSerValHisPheVal 966
|||||
1925 TCACACTGGGCTCGAGGCTCAAGAGAGGCTTCACAGAGTGTATTTCGCTT 1974
967 GlyThrGluThrSerLeuValTrpLysGlyTyrMetGlnGlyAlaIleArg 984
|||||
1975 GAAAGCGAAGGCTCTTAACTTCGAAAGAGGATATCGAAGGAGGCTATAGG 2024
983 qSERGLYILAVGLYALAAAGLVALVALASSTLQWATLFTVALIAA 1000
|||||
2025 ATCCAGGTAAGGAGAGGCTGAGAAATGAGGATACGCTGGCTGGTACGAG 2074
1000 Lq 1000
11
2075 CA 2076

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the detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed.

50 Sequence 1003 BP: 690 A; 840 C; 819 G; 654 T; 0 other;

aliquant scores:

Quantity:	5204.00	Length:	1000
Ratio:	5.204	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

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267	ThrValAlaIleAlaGluAsnGlySerThrThreonAspTyrIleGluSerProGly	284
801	CACGTGTTCAGCGCTCCACCTGCTGGTACACATGATACATCCACATCTTGACTTGA	850
284	GATArgArgValAspLeuAlaThrIleuMetAspThrIleGluIleuGluGly	300
851	TGAGAGACATCCATCTCTGGCACTCTGATGATGACACCATTCAGGAAATCCGCA	900
301	IleuGlyPheGluTyrThrLeuAspAsnValThrAlaValTyrArgSerGlu	317
901	CTGGGCTTGGACTACACGCTTGACAAACGTAACGTAACGCTTGGTACGCTTCCA	950
317	ThrAlaIleArgThrThrGlyAspIleAlaArgValProValIleuValGlyTyr	334
951	AAAGGCTGGCAGCTACACTGGATGGACATTCCTGCTGATCTGTCTCTGTCGGA	1000
334	IleValAlaAsnAspGlyIleuLeuPheValLeuGlyGluAsnAspThrThr	350
1001	CGGTGGCCCAACACAGCAGCCATTCCTCTGTCTCCGCGAGAAATGACACCGCA	1050
351	AlaTyrPheGluGluValAlaIleProSerSerIleProArgGluProGluIleIle	367
1051	GTATATCTGTGACAGAGCGAATCCCGAATCAGCCCGCAACCTTATACATACCT	1100
367	uGluGluValAlaTyrProIleGlySerProGlyTyrThrValGlySerProGluAsp	384
1101	CGTTGAGAGATATCCCATGATGGATCCGACAGCAATCGAATACGCTCAATAC	1150
384	IleIleAlaIleIleGluThrThrGluValAlaIlePheGluTyrSerThrAlaIle	400
1151	ACATTCGCCCCATTCAGACAGCGAGGATAAATATCCCATGCTCTCTCTGCTAC	1200
401	ValAlaGluAspSerArgAsnArgGluIleLeuProSerThrPheArgTyrTyr	417
1201	GTGGCTGCACGACACCGCGAAATCGGGTATACCTCTCTGGGCTATATCTA	1250
417	IleAsnAlaThrPheGluAsnLeuGluIleuPheProGlySerGluValTyrH	434
1251	CAATGGAGACCTTGGAAATCTGTAACCTTTCCCTGGGTGCTAAAGTCTAC	1300
434	IleSerSerThrValAlaGlyMetValProGlyTyrProGlyProValAlaSerAla	450
1301	ACAGGCTGTAACTGGCGGAGTGGTCTTTCGCACTACGATCGCTGGCAAGTGG	1350
451	ThrAlaLeuGluAlaGluThrSerTyrSerTyrMetGluGlyAlaThrPheAla	467
1351	ACCGCCCTTCAGACCCCAACAGCGCAAAATACATCATAGCGGTACGCTGGCGGC	1400
467	ArgPheAlaIleAspAsnProMetAsnGluProValTyrPheGluValProAsn	484
1401	CTTTGGCCAAAAACCCATGTAATGAGGCTGGTGGTGGAAACAATGGTGAAATG	1450
484	AlaAlaAlaLeuGlySerProGlyTyrSerIleLeuValAlaArgValSerPro	500
1451	TCCCGGCGCTTGGTTCATCATAGGCAAGCAATACAGATTCAGATGCTGCTCCA	1500
501	AlaThrIleAspPheIleArgValAlaLeuGlyThrAsnArgTyrThrThrGlu	517
1501	GGACACATAGACCAACGACATGGCTCTTGTATACAGGCTTATATATACAGAT	1550
517	uGlyThrIleGATArgProArgThrPheGluValGlySerGlyTyrGlySerG	534
1551	GGAGCAATACGGCGGAGAGATATTTGGGCGAGAGACGGCGAGAGGAGCG	1600
534	ValGlyValGlySerTyrAspAsnValAlaAspValValValValGluValGly	550

[illegible][illegible]

1151 AGAATGGGCGCATTTAAACCGAGGAAAGATTCAGAGCTGCTCTGCGATC 1200
 401 ValAlaGlnAspSerArgAspArgGlyIleProSerIlePargIleTyrTyr 417
 1201 GTGGCTGAGGACTGAGGAGATCGAGATCGGATCGCTCTGAGCGCTACTACTA 1250
 417 TAAAGAlaIlePheGlnAspGlnGlnGlnGlnPheProGlySerGlnValTyr 434
 1251 GAAAGGAGCTTTGAGATGCTGAGGCTTTTCCTGGGTCGCAAGTGTATC 1300
 434 LysSerSerIleValIleMetValPheGlyThrTyrProValAlaSerAla 450
 1301 AACAGCTCGAGAGTCGGAATGGCTGTTGGCAGCGATTCCTGGCAAGTGGC 1350
 451 ThrAlaGlnGlnAlaGlnThrSerLysIleMetGlnGlyAlaIlePheAla 467
 1351 ACGGCTTCAGATTCGAGAGCAAAATGATGTAAGCTGGCTGGAGCGGCG 1400
 467 APhenAlaLysAsnProMetAspGlyProGlyTyrPheLysGlnValProAsn 484
 1401 CTTTCGCAAAACCGCATGATGGGCTGGTGGAAACAGATGCGCAATG 1450
 484 AlaAlaAlaGlnLysSerProGlyLysAlaIleGlnValAlaSerPro 500
 1451 TCGAGGCGTTGCTTCACAGATCAAGCGCAATCGAGTTCAGGCTGCTGCA 1500
 501 AlaThrIleAspGlnArgGlyAlaLeuTyrThrArgTyrThrGlnGly 517
 1501 GCGAGCATACGACGAGATGATGCTGTAACGAGTATATTAACAGGTT 1550
 517 uGlyThrIleAlaProArgThrPheTyrLysSerGlyLysGlyProGly 534
 1551 GAGCAATATGATGATGATGATTTTCGCGAGAGCAAGGAGGAGAGGAGAG 1600
 534 LysGlyLysSerLysAspAspValAlaAspValValValAlaGlnVal 550
 1601 GCGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1650
 551 LeuSerGlyProGlnTyrAlaArgLysValIleAlaIleGlnGlnGln 567
 1651 TTGAGGCGGTTTGAGATGAGGATGAGGATGAGGATGAGGATGAGGATG 1700
 567 AlaValLeuGlnAlaMetAspArgValGlyLysIleLeuSerValG 584
 1701 GCGCTTTTTCAGATGATGATGATGATGATGATGATGATGATGATGATG 1750
 584 LysSerLysProGlyArgThrIleAsnAspLeuAlaAlaIlePhe 600
 1751 AATCGGCTCGCGATAGGAGGATTAACAGATGCTTCGCTGGCGGATC 1800
 601 AsnAspSerAsnGlnSerGlnValSerArgPhePheGlnArgPheIle 617
 1801 AATGATAGGAGGATGAGGAGGATGATGATGATGATGATGATGATGATG 1850
 617 uGlyLysGlnLeuGlnArgThrThrGlnLysSerIleIleGlnAlaGln 634
 1851 GAGGAGGAGGATGAGGAGGAGGATGAGGATGATGATGATGATGATGATG 1900
 634 SpGlyThrThrThrAlaProTyrGlyAspSerLeuLeuSerGlnGln 650
 1901 AGGAT 1950
 651 ValAlaSerAlaLeuAlaLeuLeuPheValIlePheSerGlnLeuIleG 667
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 2051 ACGATGTACCTTGCGGACCTACTGTCAGAGGAGGATCAAACTTGGCTGCT 2100

701 ValLeuGlyValAlaAsnGlnIleThrArgAlaLeuLeuGlyValGlnAl 717
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 2901 AATGAT 2950
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XX Sequence 2076 bp: 564 A 422 G 926 G 564 T 0 other

alignment_scores:
 quality: 4058.50 length: 1042
 pairs: 4867 gaps: 20
 Percent similarity: 75.849 Percent identity: 63.663

alignment_block:

US-09-658-835c-25 x AAZ58404

Align seq 1/1 to: AAZ58404 from: 1 to: 2976

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17 uSerAlaSerleuAlaSerleuValaProThrValIleLeuAspA 72
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51 CTGGGCGCTGCTGACAGGAGAGAGAGATTTGGGCTGCGAGAGAGCATC 100
32 IsgIyMerValValIleIyThrThrThrValIleProGlyThrThrAlaThr 48
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101 TGGGCGAG.....GTTGAGGAGCTGGGCGGAG 129
49 ValSerGlyPheLeuGlyValProPheAlaAlaSerProThr..... 62
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63 ArgPheAlaProThrThrAlaProValProIleProThrProLeuGlnA 79
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180 GGTTCGCAAGGCGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 229
79 IatThrAlaIyGlyProAlaGlyProLeuLeuPheAsnIyProGlyGlu 95
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96 IeuAlaProIleIleThrPheAlaIleThrPheAsnIleProProSerAla 112
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112 IctIleGCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 128
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223 eAlaIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 239
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447 alAlaSerAlaIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 463
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464 AlaIyPheAlaIyPheAlaIyAsn.....ProMetAs 474
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[illegible][illegible]

[illegible][illegible]

XX 004: Eukaryotic microflora.

Seq: Sequence: 4591 bp; 758 A; 1017 C; 1064 G; 752 T; 0 other.

alignment_scores:

GapPenalty: 2961.50
Ratio: 3.777
Percent Identity: 61.095

alignment_block:

us-09-658-835c-25 x AAZ60645

Align seq 1/1 to: AAZ60645 from: 1 to: 4591

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8 GCAAGCGACGTTGTGTGTGGACCAATCTCCAAATCGCATCTGCTC 667
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12 GGTTCAGGACGTGCGCGGAGGT 746
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XX W0902703-A1.
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 XX 21-JAN-1997.
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 XX 07-JUL-1998: 98W0-0513987.
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 XX 07-JUL-1997: 97US-0888950.
 XX 07-JUL-1997: 97US-0888949.
 XX
 XX (Gen.) F1000R III BRB INT INC.
 XX
 XX Brown RA, Jewick J, Gilliam JT, Maddox JR, Reed TA;
 XX W01: 1997-128904/10.
 XX P-ISBN: AAW94287.
 XX
 XX Newly isolated polynucleotides useful for degrading and detoxifying
 XX tumourists - and methods for identifying transformed plant cells
 XX
 XX claim 4: Pages 56-66; 8pp; English.

This DNA encodes a tumourin esterase from E. spilioid. This enzyme can
 degrade tumourin. The polynucleotides encoding tumourin degrading
 enzymes are useful for degrading tumourins during the process of
 harvesting grain for animal feed, or in plant tissues, which are used for
 silage or as a spray on grain. Fruit or vegetables, which are also useful
 for detoxifying tumourins, structurally related mycotoxins, and
 tumourin hydrolysis products of both. The tumourin esterase genes
 (contained within an expression cassette, encoding a tumourin
 degrading enzyme) is introduced into plant cells that are cultured on a
 medium containing a phytochrome linked to a ribozyme (ICA),
 which inactivates the phytochrome unless it is cleaved by an esterase.
 The polynucleotides are also used in a method for measuring gene
 expression, comprising transforming cells with the esterase gene
 operably linked to a promoter, adding substrate, and measuring the level
 of hydrolysed product. The isolation of the polynucleotides encoding the
 tumourin degrading enzymes permits the degradation and detoxification of
 tumourins, which are toxic and potentially widespread in food and feed.

Sequences 1947 BP: 448 A: 595 G: 497 C: 477 T: 9 Effect.

alignment_scores:

Query: 2660-59	Length: 542
Ratio: 5.068	Gaps: 3
Percent Similarity: 96.863	Percent Identity: 94.096

alignment_block:
 US-09-658-835C-25 x AAX05730 ..

Align seq 1/1 for AAX05730 from 1 to 1937

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1 MetAlaAsnLysHisLeuSerLeuSerLeuPheLeuValLeuLeuIle 17
111 :::::::::::::::::::: ::::::::::::::::::::
155 AAGCGGATGAGAGATATACGCTGCTGCTGCTGCTGCTGCTGCTGCT 202
171 ucst.....AlaSerLeuAlaSerCysAlaProThrValIleAsp 32
171 :::::::::::::::::::: ::::::::::::::::::::
238 TCTTTTTCATCAATATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 252
32 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 48
32 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 48
254 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 302
43 ValSerLysPheLeuValProPheAlaAlaSerProThrPheAla 65
43 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 65
403 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 352
45 atProThrPheAlaProValProThrPheProLeuGlnAlaIleAla 82
45 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 82
453 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 402

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82 YGSLProAlaLysProAlaLysProAlaLysProAlaLysProAlaLys 98
82 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 98
403 ATGCTGACAGCATGCTGACAGCATGACAGCATGACAGCATGACAGCAT 452
99 MetProAlaLysProAlaLysProAlaLysProAlaLysProAlaLys 115
99 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 115
454 ATGCTGACAGCATGCTGACAGCATGACAGCATGACAGCATGACAGCAT 502
115 GAGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCG 132
115 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 132
503 GAGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCG 552
122 YGSLProAlaLysProAlaLysProAlaLysProAlaLysProAlaLys 148
122 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 148
553 AAGCGGATGAGAGATATACGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
149 SerPheHisLeuValProPheAlaAlaSerProThrPheAlaIle 165
149 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 165
603 TATTCATGCTTTCATGCTTTCATGCTTTCATGCTTTCATGCTTTCAT 652
165 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 192
653 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 702
182 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 198
182 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 198
754 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
199 ATGCTGACAGCATGCTGACAGCATGACAGCATGACAGCATGACAGCAT 215
199 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 215
755 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 802
215 YGSLProAlaLysProAlaLysProAlaLysProAlaLysProAlaLys 242
215 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 242
863 AAGCGGATGAGAGATATACGCTGCTGCTGCTGCTGCTGCTGCTGCT 852
232 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 248
232 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 248
863 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 902
249 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 265
249 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 265
903 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 952
255 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 292
255 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 292
953 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1002
282 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 298
282 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 298
1003 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1052
299 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 315
299 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 315
1053 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1102
315 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 342
315 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 342
1103 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1152
332 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 348
332 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 348
1153 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1202
349 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 365
349 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 365
1203 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1252
365 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 382
365 TGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 382
1253 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1302

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[illegible]

11 New isolated polyglutamate, polyphenols and polyphenols are used for detecting and
p1 degrading fumonisin or structurally related mycotoxin in processed
p1 grain or in silage -
xx
xx
xx Example 10, Page 97-100; 154pp; English.
xx
xx The present sequence is that of the coding region of full-length
xx amino polyol amine oxidase (APAO) cDNA of *Periplasma sp.*
xx 214110. APAO is capable of degrading fumonisin. It is hydrolysis
xx product API, and related mycotoxins. The invention provides APAO
xx polyglutamates (see A252381-53) and polyphenols (see A256400-05)
xx *E. coli* and *Shigella* and *Shigella* atrovivax. The polyglutamates are
xx used to transform plant cells normally susceptible to fusion or
xx other toxin-producing fungus infection. Transgenic plants can be
xx regenerated from the transformed plant cells. Also provided are
xx methods for expressing both APAO and a fumonisin-esterase in a
xx transgenic plant, and for producing APAO enzyme in prokaryotic and
xx non-plant eukaryotic systems. Transgenic plants are capable of degrading
xx fumonisin or of producing the degrading enzymes are provided.
xx Methods for detoxification of grain, grain processing, silage, food
xx crops and in animal feed and human microorganisms are also disclosed.
xx APAO polyglutamate is also useful as a selective marker.
xx
xx Sequence 1804-1824 A: 501-502 (576-7) 0 other?

[illegible]

XX Cnstra op. Envis 1. Polymers G. Gilliam JT. Madrox JB.
 XX WP1: 2000-102126-016
 XX P-PSDB: AAV68849.
 XX
 PT New nucleic acid encoding aminopolylamine oxidase, used, e.g. to
 PT generate plants resistant to Fusarium.
 PS
 XX Example 10: Page 99-101, 145pp, English.
 XX
 CC The present sequence encodes a full length *Exophiala spinifera*
 CC aminopolylamine oxidase (APO). The enzyme has homology to the
 CC flavin containing oxidoreductase family that oxidize primary amine
 CC to an aldehyde or ketone, releasing ammonia and hydrogen peroxide.
 CC The APO enzyme derives energy from the oxidation of plant
 CC plant's destruction of mycelium by APO generates, as a by-product,
 CC hydrogen peroxide which is itself an antimicrobial and stimulates the
 CC plant's own defense systems. The APO polynucleotides are used to
 CC generate plants (particularly maize) that are resistant to Fusarium or
 CC other fungi that produce mycotoxins and/or to degrade such mycotoxins
 CC (e.g. during ensiling); for recombinant production of APO
 CC polypeptides; as selection markers for plant transformation; and to
 CC isolate related sequences from other organisms. The APO polypeptides
 CC are used to treat mycotoxins in plant materials, including expression
 CC in engineered bacteria and fungi, e.g. rumen microflora.
 XX

Sequence from bp: 424 to 509 of 509 bp, 0 other:

alignment_scores:

Quality: 2722.50 Length: 633
 Ratio: 4.455 Gaps: 7
 Percent Similarity: 81.934 Percent Identity: 77.833

alignment_block:

us-09-658-835c-25 x AAV60641

Align seq 1/1 to: AAV60641 from: 1 to: 1803

373 LLEGLYSCFTTGGYGLLEGYSERF.....GHSAPGNIILEAL 387
 22 ATRAAATGCCCAAGGCGGCTGGCAAGAGGTAATTCACGCGGCGT 71
 387 alleglthrvalatpaphedgincysproseralailevalaia 404
 72 AGGTCACAGCAATATATATATATATATATATATATATATAT 121
 404 SPSEATATASNAATPGLYILEPROSERTFATATYTYTYTASAL 420
 122 ACGCTTCGGCGGTACAGACGCTGGCTACAGCAACAGCTGGCA 171
 421 Phegluasleuglu.....leupheproglisercluvallyth 434
 172 TTGGCCATCTGGACGCTTGGCTTGGCACTGGACGCTTCGAA 221
 434 sserSerAlvalalelmetValPheglYthTYTProValAlaser 451
 222 CGTCACCAAGATCAATATATATATATATATATATATATAT 271
 451 brAlaLeugluAlaInThrSerLysIleMetGlnGlyAlaTrp 467
 272 CCGCAATTGA.....GATGGCTCAAGCGTACG 300
 468 PheAlaLysAlaPheMetAlaSerLysIlePheGlnValProAsn 484
 301 TTTCGCTTACAGATC.....CTTCCTTCACGCTGGTGGCA... 341
 484 AlaAlaIleGlnGlySerProGlyLysAlaIleGlnValAspVal 501
 342 GTCGGCTTCCTTCACGATCAATATATATATATATATATAT 387
 501 laInrIleAspGlnIleGlyAlaIleThrAlaGlyTYTThrGln 517

387 387
 518 GLYTHDIALAFRAAGTHPHEGLYGLYSERGLGLYSERGL 534
 388 69 401
 534 YGLYGLYSERLYSPASNAVALAASPVALVALVALVALGLVAL 551
 402 ATAAATATATATATATATATATATATATATATATATATAT 451
 551 PSEASERLYSPASNAVALAASPVALVALVALVALGLVALGLYS 567
 452 LCAATATATATATATATATATATATATATATATATATAT 501
 568 LCAVALLEUVALAALASPAVALGLYGLYGLYSERLYSPAS 584
 502 CTATCTTCATATATATATATATATATATATATATATATAT 551
 584 USGLYTHGLYVALYTHDIALASNAASPGLYVALAALPLLA 601
 552 ATCGGCTCCCGGACGACGATATCAACGACCTCGGCTGGAT 601
 601 SPSEASERLYSPASNAVALAASPVALVALVALGLVALGLYS 617
 602 ATGATAGGATCAAAATGATATATATATATATATATATAT 651
 618 GLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLY 634
 652 GAGGCGAGCTCCAGAGGACATGGAAATCAATCAATCAATCA 701
 634 POLYTHDIALAFRAAGTHPHEGLYGLYSERGLGLYSERGL 651
 702 CAAATATATATATATATATATATATATATATATATATAT 751
 651 AIAASERALALASNAVALAASPVALVALGLYGLYGLYGLY 667
 752 TTGTAAGATATATATATATATATATATATATATATATAT 801
 668 GLHISERLYSPASNAVALAASPVALVALGLYGLYGLYGLY 684
 802 GATATATATATATATATATATATATATATATATATATAT 851
 684 PSEASERLYSPASNAVALAASPVALVALGLYGLYGLYGLY 701
 852 GATATATATATATATATATATATATATATATATATATAT 901
 902 LITGATATATATATATATATATATATATATATATATATAT 951
 718 HISGLISERLYSPASNAVALAASPVALVALGLYGLYGLY 734
 952 CAGGATATATATATATATATATATATATATATATATATAT 1001
 734 YLEUSERLYSPASNAVALAASPVALVALGLYGLYGLYGLY 751
 1002 LITGATATATATATATATATATATATATATATATATATAT 1051
 751 YSLYTHGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLY 767
 1052 GCAAAATATATATATATATATATATATATATATATATAT 1101
 768 PROGLYSERLYSPASNAVALAASPVALVALGLYGLYGLY 784
 1102 GATATATATATATATATATATATATATATATATATATAT 1151
 784 ASERLYSPASNAVALAASPVALVALGLYGLYGLYGLYGLY 801
 1152 ATCGGCTCCCGGACGACGATATCAACGACCTCGGCTGGAT 1201
 801 YSVALVALVALVALVALVALVALVALVALVALVALVALVAL 817


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403 GluAspSerArgAsnArgGlyLeuProSerTrpArgTyrTyrAsnAl 419
|||||
805 CAAGAGCGCTTCGGACGCTACACAAACCGCTGACAGAAACAGGTTGCCCA 854
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419 alhrPheGluAsnLeuGlu.....LeuPheProGlySerGluValT 433
|||||
845 AACATTCGACCAAAATTCGAGCTTCGCTGGCGGACCTGGACCACTTCAA 904
|||||
433 YTHSSerSerGluValAluGlyMeValPheGlyThrTyrProValAlaSer 449
|||||
905 AGCAGATGACCAACAGAGCAATACCAACGCTGGACAGGCGCCGACGAAA 954
|||||
450 AlrThrAlaLeuGluAlaGluThrSerLysThrTolGlyValAlaIlePAl 466
|||||
955 CTCACCGCAATTCGA.....CATGGCTGGAAGC 983
|||||
466 AlaPheAlaAlaLysAsnProMetAsnGlyTyrGlySerGlyValTyrCA 483
|||||
984 TACTTTGGGCTTCACAAAGCTC.....CGCTTCGACGCTGGTGGCA 1026
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483 snValAlaAlaLeuGlySerThrGlyTyrGluAlaGluGluValAlaPValSer 499
|||||
1027 ..GTCGAGCGCTGGCTTCACAGGCAATACCTGCTTCAGGCTTCAGGCAAG 1074
|||||
500 ProAlaThrIleAspGluAlaGlyAlaLeuGlyThrArgTyrTyrThrGl 516
|||||
1074 ..... 1074
|||||
516 GLeuGlyThrIleAsnProMetArgGluGluGlyTyrGlySerGlyGlyLys 533
|||||
1075 .....GGGCTGGTGGC..... 1086
|||||
533 eroGlyLysGlySerGlyAspAsnValAlaAspValValValGlyValA 549
|||||
1087 ..CGACACACACACACACACACACACACACACACACACACACACACAC 1134
|||||
550 GYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIY 566
|||||
1135 GGGCTTCAGCGGCTTCGAGAGCGGACCAACGCTCACCGCGCTGGTC 1184
|||||
566 rGylLeuValIleuGluAlaMetAspArgValGlyLysThrLeuSerV 583
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1185 CTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1234
|||||
583 alrAsnSerGlyProGlyArgGlnTrpIleAsnAspLeuGlyAlaAlaTrp 599
|||||
1235 TACAGACCGGCTTCGAGAGCGGACCAACGCTCACCGCGCTGGTC 1284
|||||
600 IleAsnAspSerAsnGlnSerGlyValSerArgLeuPheGluArgPheH 616
|||||
1285 ATTCGACACACACACACACACACACACACACACACACACACACACAC 1334
|||||
616 slenGluGlyGluGluGluArgThrThrIleAsnSerIleHisGluAlaG 633
|||||
1335 TTTCGAGAGCGGCTTCGAGAGCGGACCAACGCTCACCGCGCTGGTC 1384
|||||
633 lhrGlyGlyThrThrThrAlaArgGlyGlyAspSerLeuLeuSerGlu 649
|||||
1385 AACAGAGTAAACAACTAACTAACTAACTAACTAACTAACTAACTAACTAA 1434
|||||
650 GluValAlaSerAlaLeuAlaIleLeuLeuProValIlePserGluLeuI 666
|||||
1435 GAGCTTCGAGAGCGGCTTCGAGAGCGGACCAACGCTCACCGCGCTGGT 1484
|||||
666 cglGluIleHisSerLeuGluGluAspLeuLysAlaSerProGluAlaLysAla 683
|||||
1485 CGAAGAGCATAGCTTCGAGAGCGGCTTCGAGAGCGGCTTCGAGAGCGG 1534
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683 enAspSerValSerPheAlaHisGlyGlyGlySerGlyGlyGlyGlyGlyGly 699
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1535 TCACAGCTGGCTTCGAGAGCGGCTTCGAGAGCGGACCAACGCTCACCTG 1584
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700 AlaValIleuGlyValAlaAlaAsnGlnIleThrArgValAlaLeuLeuGlyValGl 716
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1585 GCTGCTTCGAGAGCGGCTTCGAGAGCGGCTTCGAGAGCGGCTTCGAGAG 1634
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716 uAlaHisGluIleSerMetLeuPheLeuThrAlaPtyIleLysSerAlaIat 733
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1635 AGCTACGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1684
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733 hrGlyLeuSerAsnIlePheSerAspLysGlyAspGlyGlyGlyGlyGly 749
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1685 CCGCTTCGAGAGCGGCTTCGAGAGCGGCTTCGAGAGCGGCTTCGAGAG 1734
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750 ArgGlyLysThrGlyMetGlySerIleGlyHisAlaMetSerGlySerG 765
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1735 CGATGCAAAACAGATATGCAATGCAATGCAATGCAATGCAATGCAATG 1784
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766 uValProGlySerValHisLeuAsnThrProValAlaGluIleGluHis 783
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1785 TGTTCGAGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1834
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783 eAlaSerGlyCysThrValAlaSerAlaSerGlyAlaValAlaPheArgSer 799
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1835 CGGCAATGAGAGCGGCTTCGAGAGCGGCTTCGAGAGCGGCTTCGAGAG 1884
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800 LysLysValValAlaSerLeuProThrThrLeuTyrProThrLeuThrPh 816
|||||
1885 AAAAGCTGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCG 1934
|||||
816 eSerProProLeuProAlaGluLysGluAlaLeuAlaGluAsnSerIleL 833
|||||
1935 TTCACCACTGCTTCGAGAGCGGCTTCGAGAGCGGCTTCGAGAGCGGCT 1984
|||||
833 euGlyTyrThrSerLysIleValPheValIlePAspLysProTyrIleArg 849
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1985 TGGGCTACATATACAGATAGCTTCGATATGAGCAAACTGAGTGGTGG 2034
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850 GluGluGlyPheSerGlyValIleuGlnSerSerCysAspProIleSerPh 866
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2035 GAACAGAGCTTCGAGAGCGGCTTCGAGAGCGGCTTCGAGAGCGGCTTC 2084
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866 eAlaIatArgPheThrSerIleAspValAspArgGlnTrpSerIleThrCysP 883
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2085 TGCACACATACATATGAGAGCGGCTTCGAGAGCGGCTTCGAGAGCGG 2134
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883 hemeValGlyAspProGlyArgLysPserGlnGlnSerLysGluVal 899
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2135 TATGCTTCGAGAGCGGCTTCGAGAGCGGCTTCGAGAGCGGCTTCGAGAG 2184
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900 ArgGluLysSerValTrpAspGluLeuArgAlaAlaTyrGluAsnAlaGl 916
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2185 GAGAAAACTGCTTCGAGAGCGGCTTCGAGAGCGGCTTCGAGAGCGGCT 2234
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916 ValGluGlyValProGluProAlaAsnValLeuGluThrLeuIlePserLysG 933
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2235 GAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 2284
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933 lncGlnTyrPheGlnGlnValAlaProSerAlaValTyrGlyLysAsnAspLeu 949
|||||
2285 AGCAGTATATTCGAGAGCGGCTTCGAGAGCGGCTTCGAGAGCGGCTTC 2334
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950 lIleThrIleGlySerAlaLeuArgThrProPheLysSerValHisPheVa 966
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2335 ATCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2384
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966 uGlyThrIleThrSerLeuValTrpIleGlyTyrMetGlnGlyAlaIleAla 983
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2385 TGGAGCGGAGAGCGGCTTCGAGAGCGGCTTCGAGAGCGGCTTCGAGAG 2434
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983 rGserGlyGlnArgGlyAlaAlaGluValValAlaSerLeuValProAla 999
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2435 GATCGGCTTCGAGAGCGGCTTCGAGAGCGGCTTCGAGAGCGGCTTCGAG 2484
|||||
1000 Ala 1000
|||||

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1325 GATGCAAAATAGCATGATGCGATTTGCCATGCCATGTCAAGCAACTT 1374
767 ValProGlySerValHisLeuAsnThrProValAlaGluIleGlnIse 783
1375 GTTCACACCTCACTGCACCTTAAATATCTGCTGCAATTGCAGAGTC 1424
783 PAlaSerGlyCysThrValArgSerAlaSerClyAlaValPheArgSerL 800
1425 GGCATCGCGGAGTACATACCATCGCGCTCCCGCGCTGTCGGAAGCA 1474
800 yslYsValValSerLeuProThrThrLeuThrProThrLeuThrPhe 816
1475 AAAAGTGGTGGTTCTGTACCCGACACCTTGATCCACCTTGACATT 1524
817 SerProProLeuProAlaGluIleAlaLeuAlaGluAsnSerIleLe 833
1525 TCACCACTCTTCCCGCTCGAAGCAAGCATTTGGCGGAAATTCATCT 1574
833 uGIYTYTYSerLysIleValPheValTPAspLysProThrParG 850
1575 GGGCTACTAAGCAAGATAGTCTTGATGGACAGACCTGGTGGCGCG 1624
850 IuGInGlyPheSerClyValLeuGlnSerCysAspProIleSerPhe 866
1625 AACAAAGCTTTCGGGGTCTCTCCATCGACCTGTACCCCATCTCATTT 1674
867 AlaArgAspThrSerIleAspValAspArgIuThrPheSerIleThrCysPh 883
1675 GCCAAGCATACCAAGCATCAGCTGATGACATGACATGCTCATCTGTT 1724
883 eMkValClyAspProGlyArgLysThrPheSerClyGlnSerLysGlnVal 900
1725 CATCTCCGAGACCGGAGACCTCTCCCAACAGTCCAAAGCAGTAC 1774
900 rGdInLysSerValTPAspGluLeuArgAlaAlaIleArgLysAsnAlaGly 916
1775 GACAAAGTGTGTGGAGCAACTCCGCGCAGCTACGAGAACCGCGG 1824
917 AluGlnValProGluProAlaAsnValLeuGluIleClyThrPheSerLysG 933
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933 uGIYTYTYPheGlnGlyAlaProSerAlaValTPArgLysAsnAspLeuI 950
1875 GCAGTATTCAGAGAGCTCCGAGCCCGCTATGGCTGAAGCATCTCA 1924
950 IeThrLeuGlySerAlaLeuArgThrProPheLysSerValHisPheVal 966
1925 TCCACTGTGGTTGGCGCTCAGAACCGCTTCAGAGTGTTCATTGCTT 1974
967 GlyThrGluThrSerLeuValTPArgLysGlyTYTMeGluGlyAlaIleAr 983
1975 GCAACCGAGAGCTTACTTTCGAAAGGCTATATGCAATGGCGCATAC 2024
983 ySerGlyGlnArgClyAlaAlaGluValValAlaSerLeuValProAla 1000
2025 ATGGGTCAACGAGGTGTGCAGAGTGTGGCTAGGCTGTGTCAGACAG 2074
1000 Ia 1000
2075 CA 2076


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1851 GAAAGGCAAGTCGACAGGACAAATGGAAATTCATATCAAAACAGAG 1900
644 SPGLVTHLHrThrAlaProLysAspSerLeuLeuSerGluGlu 650
1901 AAGGACAAACACACAGCTGCTTATGGTACCTCTTGGTTAAAGAGAG 1950
651 ValAlaSerAlaLeuAlaGluLeuLeuProValTyrSerGluLeuGlu 667
1951 GTTGGAAATGACTTGGGAAATATATGAAATATAGGCTCAAGTATGAGA 2000
667 uGluHisSerLeuHisAspLeuLysAlaSerProGluAlaLysAlaGlu 684
2001 AATACATAGGCTTCACAGCTCAAGGCAAGGCTTCACAGCAATGCGCTCG 2050
684 SPSPVAlaSerPheAlaHisTyrCysLeuLysGluLeuAsuLeuProAla 700
2051 ACATGTACGCTTCTGGACACTACTGGTAAAGCAATTAACCTTCAGCTGCT 2100
701 ValLeuGluValAlaAsuGluLeuThrArgAlaLeuLeuGluValGluAl 717
717 uHisGluHisSerMetLeuPheLeuThrAspTyrLeuLysSerAlaThrG 734
2101 GTTCTGGGCTTAGCAAAACAGATACAGATGCTCTCTCTGGTCTGCAAG 2150
2151 CCAAGCAATACGCAATCTTTTCTCAAGGATACATTAAGAGATGCGCTCG 2200
724 LysuSerAsuLeuPheSerAspLysAspGlyGlyGlyIleTyrMetArg 750
2201 GTCTACATATATTTCTGGTCAAAAGAAATGCGCGTGCATATATATGCGA 2250
751 CysGlyTyrTrpMetLeuSerGlyLeuLysSerAsuMetArgTyrGluGlu 767
2251 TGTAAATAGGATATCATGATTTGGCATGGCAATGTAAGAAACATCTGT 2300
767 LProTyrSerValHisLeuAsnThrProValAlaGluLeuGluGluGlu 784
2301 TGTAAATGATGGTACATGAAATGATGCTGCTGCAATTCAGTACGTCGG 2350
784 LAspGlyLysThrValTyrSerAlaSerGlyAlaValPheArgSerTyr 800
2351 CATCGGCTGGTACATAGGATGCGCTGCGCGGCGGCGGCGGCGGCGGAAA 2400
801 LysValValAlaSerLeuProThrThrLeuTyrProThrLeuThrPheSe 817
2401 AAGTGCATCTTCTGCTTACGCAAGGCTTCTGCTGCTGCTGCTGCTGCT 2450
817 LProProLeuProAlaGluLysGluAlaLeuAlaGluHisSerIleLeuG 834
2451 AATAGGCTTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2500
834 LysTyrTyrSerTyrLeuValPheValTyrAspLysProTyrProArgGlu 850
2501 GTTATATATATATATATATATATATATATATATATATATATATATAT 2550
851 GluLysPheSerGlyValLeuLeuLysSerSerTyrAspProIleSerPheAl 867
2551 CAAAGCTTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2600
867 AATGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2650
2601 CAAAGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2650
884 eValGluLysProGlyTyrTyrTyrSerThrHisLysLysValArg 900
2651 TGGTGGGAAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2700
901 GluLysSerValTyrAspGluGluAlaAlaLysGluHisAsuAlaLysAl 917
2701 CAAAGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2750
917 actValThrGluThrAlaAsuValLeuGluThrLeuThrSerTyrGluGlu 934
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2751 CCAAGTCCGACAGCGCGGCAAGCTTCTGCAATTCAGTACGCTTCTGCAAT 2800
934 LntTyrPheGluLysValAlaProSerAlaValTyrGluLysuAsnAspLeuLe 950
2801 AGTATTTCTGCAAGATCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2850
951 ThrLeuGlySerAlaLeuArgThrProPheLysSerValHisPheValGlu 967
2851 ACATGCGCTTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2900
967 YThrGluThrSerLeuValTyrLysGlyTyrMetGluGlyAlaLeuArgS 984
2901 AACGCGACGCTCTTACTTTGCAAAAGCGATATATGCAAGCGGCGGCGGAT 2950
984 eGlyGluArgGlyAlaAlaGluValValAlaSerLeuValProValAla 1000
2951 CAGATTCACGCAAGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3000
seq_name: 6/4/1994, 6/2/1994, 6/2/1994, 6/2/1994, 6/2/1994
seq_documentation_block:
? Sequence 24, Application US/09-62168A
? Patent No. 6211435
? GENERAL INFORMATION:
? APPLICANT: Crasda, Oswald R.
? APPLICANT: Durick, Jonathan P.
? APPLICANT: Folkerts, Otto
? APPLICANT: Gilliam, Jacob T.
? APPLICANT: Maddox, Joyce R.
? TITLE OF INVENTION: Antimicrobial Polypeptides and Related Polypeptides and Methods of Use
? FILED PERCENT: 0875
? CURRENT APPLICATION NUMBER: US/09-62168A
? EARLIER FILING DATE: 1999-07-12
? EARLIER APPLICATION NUMBER: 60/092,936
? NUMBER OF SEQ ID NOS: 33
? SOFTWARE: FASTSEQ for Windows Version 3.0
? SEQ ID NO 24
? LENGTH: 3003
? TYPE: DNA
? ORGANISM: Unknown
? FEATURE:
? OTHER INFORMATION: Sequence is a barley alpha amylase signal
? Patent No. 6211435
? OTHER INFORMATION: and K:LIAPAO
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: (1)...(72)
? OTHER INFORMATION: Barley alpha amylase signal sequence
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (73)...(1575)
? OTHER INFORMATION: esp1 mat
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1576)...(1611)
? OTHER INFORMATION: spacer sequence
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1612)...(3000)
? OTHER INFORMATION: K:LIAPAO
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)...(3000)
? NAME/KEY: misc_feature
? LOCATION: (1612)...(1614)
? OTHER INFORMATION: Extra lysine
? US 09 352 168 24
alignment_scores:

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Quality:	5204.00	Length:	1000
Ratio:	5.204	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

adament_block;
115-00-353-168-24

At the end of 1971 to: 45-09-352-168-24 From: 1 to: 3003

[illegible][illegible]

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1701  CCGCGCTCTTGACCGAATGATGATGCTAGGGGAAACATCTGAGGTGATG 1750
584  InsertProteinValThrThrThrAspSerLeuValAlaAlaThrPhe 1800
1751  AATCGATGCTGGCGAGGACGACATCAAGCAATCTGGGCGCTGGCGTGGATC 1800
601  AspAspSerAsnGlnSerGluValSerArgLeuPheLeuArgPheHisLeu 617
1801  AATGATGATGACCAACCAAGCAAGATATGAGATGCTGTTGAAGATTTGATT 1850
617  GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 634
1851  GGAAGGAGAGGCTGAGAGCAAGATGAAATTCATATCAACACCAAG 1900
634  SPGLYTHRTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT 650
1901  ACGGATGACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1950
651  ValAlaSerAlaLeuAlaGluLeuLeuProValTTPSerGlnLeuLeuLeu 667
1951  GTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2000
667  GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 684
2001  ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2050
684  SPGLYTHRTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT 700
2051  ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
701  ValLeuValAlaAlaSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 717
2101  GTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2150
717  AATCGATGCTGGCGAGGACGACATCAAGCAATCTGGGCGCTGGCGTGGAT 734
2151  CCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2200
734  LysLeuSerAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 750
2201  GTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2250
751  CysLeuSerAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 767
2251  TCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2300
767  LysLeuSerAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 784
2301  TCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2350
784  LysLeuSerAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 800
2351  CCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
801  LysValValAlaValSerLeuProLeuLeuLeuLeuLeuLeuLeuLeuLeu 817
2401  AATCGATGCTGGCGAGGACGACATCAAGCAATCTGGGCGCTGGCGTGGAT 2450
817  ProProLeuProAlaGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 834
2451  ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2500
834  LysLeuSerAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 850
2501  CCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2550
851  GlnGlySerAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 867
2551  CCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2600
867  AATCGATGCTGGCGAGGACGACATCAAGCAATCTGGGCGCTGGCGTGGAT 2650
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2601  CAGACATACCGACATGACGATGATGATGATGATGATGATGATGATGATGAT 2650
884  eValGlyAspProGlyLeuGlyTTPSerGlnGlnGlnGlnGlnGlnGlnGln 900
2651  TGGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700
901  GlnGlySerValTTPAspGlnLeuAlaAlaAlaAlaAlaAlaAlaAlaAla 917
2701  TAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2750
917  GlnValProGlnProAlaAlaSerValLeuLeuLeuLeuLeuLeuLeuLeu 934
2751  CCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2800
934  LysLeuSerAlaLeuAlaProSerAlaValTTPGlyLeuAspSerLeuLeu 950
2801  AGTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2850
951  ThrLeuGlySerAlaLeuAlaThrProPheGlySerValHisPheValG 967
2851  ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2900
967  ThrLeuThrSerLeuValTTPGlyTTPMetGlnGlnGlnGlnGlnGlnGln 984
2901  ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2950
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2951  CCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000

seq_name: /cqr2_6/p/udata/2/ina/64/comb.seq.us-09-652-152-28

seq_documentation_block:
: sequence 28, Application US/09152159A
: Patent No. 6211434
: GENERAL INFORMATION:
: APPLICANT: DuPont, Jonathan P.
: APPLICANT: Gilliam, Jacob T.
: TITLE OF INVENTION: Amino Polycl Amine Oxidase
: FILE REFERENCE: 1134
: CURRENT APPLICATION NUMBER: US/09/352,159A
: EARLIER FILING DATE: 1998-07-12
: EARLIER FILING DATE: 1998-07-25
: EARLIER APPLICATION NUMBER: 60/135,391
: EARLIER FILING DATE: 1999-05-21
: NUMBER OF SEQ. ID NOS: 46
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ. ID NO 28
: LENGTH: 3618
: TYPE: DNA
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: gsf:espl:sp_k:trapo: 3618 1-687, gsf:
: OTHER INFORMATION: polylinker: 2390, espl mat: 2191-2226, spacer:
: OTHER INFORMATION: 2227-3615, K:trapo, 3616-4618, stop codon. For
: OTHER INFORMATION: bacterial expression.
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(687)
: NAME/KEY: misc_feature
: LOCATION: (1)...(687)
: OTHER INFORMATION: gsf + polylinker
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: (688)...(2190)
: OTHER INFORMATION: espl mat
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (2191)...(2226)
: OTHER INFORMATION: spacer sequence

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FEATURE:
 NAME/TYPE: misc_feature
 LOCATION: (2227)...(3615)
 OTHER INFORMATION: K:ETAPAO
 FEATURE:
 NAME/TYPE: misc_feature
 LOCATION: (2227)...(2229)
 OTHER INFORMATION: Extra lysine
 OS: 09-658-159-28

alignment_scores:
 Quality: 5099.00 Length: 1016
 Ratio: 5.130 Gaps: 2
 Percent Similarity: 37.835 Percent Identity: 96.752

alignment_block:
 OS-09-658-835C-25 x OS-09-352-159-28

Align seq 171 to OS-09-352-159-28 from 1 to 3618

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3 AsnLysHisLeuSerLeuSerLeuPheLeuVal...LeuLeuGlyLe 17
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568 GATTAAGTACTTCAATCCAGCAAGATATAGCAATGGCTTGGACGCTG 617
17 GSEALASCTLeuAlaSerGly..... 24
|||||.....|
618 GCAAGCAGCGTTGGTGTGTACCAATCCCAAAATCGATCGTTC 667
25 ..... AlProThrValLysHisPheLeuGlyMet 34
|||||.....|
668 GGGCTGATCCCGGAATTCGCTCTACTGTCAAGATTGATGCTGGATG 717
45 ValValGlyThrThrThrValProGlyThrThrAlaThrValSerG 51
|||||.....|
718 CTGTGGGACCACTACTACTACTGTCGACCACTGCGACCGCAACGA 767
51 UpheLeuGlyValProPheAlaLeuSerProThrArgPheAlaProPro 68
|||||.....|
768 GTTCTTGGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 817
68 hTrpGProValProLysPheThrProLeuGlnAlaThrAlaTyrGlyPro 84
|||||.....|
818 CTGTCGCGGCTTGGTGGTCAACGCGCTTGGTAAGCCACTGCATATGTC 867
85 AlaGlySerGlnGlnProPheAsnTyrProGlnGlnLeuArgGlnLeuPhe 101
|||||.....|
868 GCAATGCTCAACCAATTCAATTACCCGCAAGACACTCCGAGATTCGAT 917
101 LAlaThrPheLeuSerThrProProSerAlaGlyGlySerGlnAspGly 118
|||||.....|
918 GGGCTGTTTAAATATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 967
118 GAspLeuAsnLeuLeuValTyrGlyThrGlnLeuSerThrAsnGlyAlaVal 134
|||||.....|
968 TGAACCTCAACATCTAGCTCCAGAACCTGAGAACCAAAACAAGCCCTC 1017
135 MetValTyrPheLeuTyrGlyValAlaLeuGlyTyrGlyTyrPheAsnSerPhe 151
|||||.....|
1018 ATGCTTTCATATACCTCGACCTGAGCTTGGCAATATGCTTGGAAATTCAT 1067
151 SLeuTyrAspGlyAlaSerProValAlaAspGlnAspValAlaValTyr 168
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1068 CCTTACAGCGCTCTATTTCGTAACCAATAGCATGCTATCGCGCGGA 1117
168 hTrpLeuAsnTyrArgTyrAspGlyGlyGlyPheThrAlaAlaProGlnLeu 184
|||||.....|
1118 GATCAACATACGAGAACACATTCGCGCTTCTCTCTCTCTCTCTCTCTCT 1167
185 ProLeuThrGlnArgAsnLeuGlyPheLeuAspGlnArgPheAlaLeuAs 201
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1168 GCAATATACAGCAAGAAATCTCCGCTCCCTAGACCAAAAGTTTCTTTGGA 1217

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201 PTrPValGlnArgAsnLeuAlaAlaPheGlyGlyAspProArgGlyValT 218
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218 hTrpLeuPheGlyGlySerAlaGlyValArgSerValAspValLeuLeuThr 234
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1268 CAATATTTGGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1317
235 SerMetProHisAsnProLeuPheArgValAlaAlaLeuGlySerGlyVal 251
|||||.....|
1318 TCTATGCCACACACACCCACCTCTCGAGCAGCAATCATGGGTGCGGGGT 1367
251 LAlaSerTyrAsnProPheProGlySerAspLeuSerGlyArgProPheSer 268
|||||.....|
1368 GGGTACTACAACTTCCCAAGGAGATTTTCCGACCTTGGAAACCA 1417
268 hValGlnAlaLeuAsnGlyThrThrSerLeuAspProLeuSerGlyMet 284
|||||.....|
1418 CTTTCACAGCTCTCAACTGTAACACAGATATGACATCTTCACTGTATG 1467
285 ArgArgValAspLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 301
|||||.....|
1468 AGAAGAGTGAATCTTACACTCTTAAGACAGATGAGACCACTGGAGCT 1517
301 GcLysPheGlyTyrThrLeuAspAsnValThrAlaValTyrArgSerGln 318
|||||.....|
1518 TGGGTTTAGTAGTACGCTTGGACACAGCTAAGCGCTGTACCACTTCGAAA 1567
318 hTrpAlaArgThrThrGlyAspLeuAlaGlyValProValLeuValGlyThr 334
|||||.....|
1568 CGGCTGGACAGATGAGTACATGCTGCGTACGCTGCTGCTGCTGCTGCT 1617
335 ValAlaAsnAspGlyLeuLeuPheValLeuGlyGlyLeuAsnAspThrGlnAl 351
|||||.....|
1618 GTGGGCAACAGCAGGACTCTCTTCTCTCGCGCAGAAATGACACCCAGAC 1667
351 ArgTrpLeuGlnGlnAlaLeuProAsnGlnPheAspLeuTyrGlnThrLeu 368
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1668 ATATCTTCAAGTAAATGATGATGATGATGATGATGATGATGATGATGAT 1717
368 GlnGlyAlaGlyTyrProLeuGlySerPheGlyGlyGlySerProLeuAspGln 384
|||||.....|
1718 TTGGACATATCCCATTCGATTCGCCAGGATCCGATCCGCTCAAGATGAG 1767
385 LLeuAlaAlaLeuLeuThrGlnValArgPheGlnGlySerProSerAlaLeuVal 401
|||||.....|
1768 ATGGCCGCAATGAGACCGAGGTAAAGATTCAGTGGCTGCTGCTGCTGCT 1817
401 LAlaGlnAsnSerArgAsnAlaGlyTyrProSerThrPheTyrTyrPhe 418
|||||.....|
1818 GGGCTGAGGAGTCCCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 1867
418 SAlaThrPheGlnAsnLeuGlnLeuPheProGlySerGlnValTyrThr 434
|||||.....|
1868 ATGGACCTTTGAGAACTCGAGCTTTCCCGGCTCCCAAGCTGACACAG 1917
435 SerSerGlyValGlyMetValLeuPheGlyTyrTyrProValAlaSerAlaThr 451
|||||.....|
1918 AGCTCTGAAGTGGGATGGTGTGTGGACCAATCTCTCTCTCTCTCTCTCT 1967
451 LAlaLeuGlnAlaGlnLeuSerLysTyrMetGlnGlyAlaThrPheAlaAla 468
|||||.....|
1968 GGGCTGAGAGGAGTAAAGAGGAGTAAATACATATGAGGAGGAGGAGGAG 2017
468 hValAlaAsnProMetAsnGlyTyrGlyTyrPheGlnValProAsnVal 484
|||||.....|
2018 TTCCCAAAAACCCCAATGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 2067
485 LAlaAlaLeuGlySerProGlyTyrAlaAlaLeuValAspValSerProAl 501
|||||.....|
2068 GCGGAGTCTTGGCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2117
501 aThrLeuAspGlnArgGlyAlaLeuTyrThrArgGlyTyrThrGlnLeu 518

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OTHER INFORMATION: 2227-3615, K122ALV, extra lysine 4016-4678, stop
OTHER INFORMATION: codon for bacterial expression
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3615)
NAME/KEY: misc_feature
LOCATION: (1)...(467)
OTHER INFORMATION: qast + polylinker
FEATURE:
NAME/KEY: misc_feature
LOCATION: (688)...(2190)
OTHER INFORMATION: espi mat
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2227)...(2226)
OTHER INFORMATION: spacer sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2227)...(3615)
OTHER INFORMATION: K122ALV
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2227)...(2229)
OTHER INFORMATION: Extra lysine
US-09-658-168-28

alignment_scores:
Quality: 5099.00 Length: 1016
Ratio: 5.130 Gaps: 2
Identity: 97.835 Percent Identity: 96.752

alignment_block:
US-09-658 835c 25 X US-09-352-168-28
Align: 361 1/1 100 98-09-352-168-28 from: 1 to: 3618
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568 GATTAATCTTCAATTCAGTAAGTAATATAGCATGCGCTTTCAGAGCGCG 617
17 uSerAlIserLeuAlaSerGly..... 24
618 GCAAGCGACGTTGGTGGTGGCGACCAATCCCAAAATCGCATCGGTTTC 667
25 .....AlaProthrValIysIleAspAlaGlyMet 34
608 CCGCTGGATCCCGAATTCATCTGATCTGATCTGATCTGATCTGATCTG 717
45 ValValGlyThrThrThrValProGlyThrAlaThrValSer31 51
718 GTGGTGGCGACGACTACTACGCGCGCGCGCGCGCGCGCGCGCGCGCG 767
51 uPhleuGlyValProPheAlaIleSerProThrAlaPheAlaProPro 68
768 GTTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 817
68 hArgProValProTTPSerThrProLeuGlnAlaThrAlaTyrGlyPro 84
818 GTGGTGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 867
85 AlaGlyProGlyGlyAlaPheAsnTyrProGlyGlyLeuAlaGlyGly 101
868 GCAAGCGACGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 917
101 AlaAlaPheAsnThrProProSerAlaGlyIleSerGlyAspCysLeu 118
918 GCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 967
118 uAsnLeuAsnIleTyrValProGlyThrGluAsnThrAsnIleValAla 134
968 TGAAGCTCAACATCTAGCTGGCGAGGAGGAGGAGGAGGAGGAGGAGGAG 1017

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125 MetValITPLeuSerGlyValAlaLeuGlyThrGlyTTPAsnSerPheH 151
1018 ATGGCTTGGATATATGCTGGAGCGCGGAGATATGATGATGATGATGAT 1067
151 sleuTyrAspGlyAlaSerPheAlaAlaAsnGlnAspValIleAlaValT 168
1096 CTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1117
168 hTlleAsnTyrArgThrAsnIleLeuGlyPheProAlaAlaArgGlnLeu 184
1118 CCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1167
185 ProIleThrGlnAlaGlnLeuGlyPheLeuAspGlyArgPheAlaLeuAs 201
1104 CCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1217
201 PTPValGlnAlaGlnIleAlaAlaPheGlyGlyAspProValGlyValT 218
1218 GTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1267
218 hTllePheGlyGlnIleSerAlaGlyGlyArgSerValAspValLeuLeu 234
1268 CAAATATTTGGGCGAGATGCTGGGCGCGAGAGTGTGCGACCTGCTGACG 1317
235 SerMetProIleAsnProProPheAlaAlaIleMetGlnSerGlyVal 251
1318 TCAATGCCACCAACCCACCTCCGACGACGACATATGATGATGATGATG 1367
251 AlaAsnTyrAsnProPheProGlyGlyAspLeuSerGlyProTTPAsnThr 268
1368 GCGTAACTACACTTCCCAAGGAGATTTGTCGCAACCTGGAACACCA 1417
268 hValGlnAlaIleAsnCysThrThrSerIleAspIleLeuSerCysMet 284
1418 CTTTTCAGGCTGCAACCTGACACGATACACGATACACGATACGATACG 1467
285 ArgArgValAspLeuAlaThrLeuMetAsnThrIleLeuIleLeuGlyLe 301
1404 ACAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1517
301 uGlyPheGlyThrThrLeuAspAsnValThrAlaValTyrArgSerGly 318
1518 TGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1567
318 hValAlaGlyThrThrGlyAspIleAlaArgValProValLeuValGlyThr 334
1568 CGGCTGGCGACGACGATGATGATGATGATGATGATGATGATGATGATG 1617
335 ValAlaAsnAspGlyLeuLeuPheValIleuGlyGlnAsnAspThrGlnAl 351
1618 GTGGCGAAGCGAGGAGCTTCTTCTGCTCGCGGAGAAATGACACCGAAG 1667
351 ATyrLeuGlnGlnAlaIleProAsnGlnProAspLeuArgGlnThrLeu 368
1668 AATATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1717
368 LeuGlyValTyrProIleGlySerProGlyIleGlySerProGlnAspGln 384
1718 TTGGAGCATATCCATTGATGATGATGATGATGATGATGATGATGATGAT 1767
385 IleAlaAlaIleGlnThrGlnValAlaArgPheGlnCysProSerAlaIle 401
1768 ATGGCGGCATTGAGACGAGGAGGATGAGATTCATGCTCTTCTGCGCAT 1817
401 AlaAlaAspSerAlaAsnAlaGlyIleTyrSerTTPArgTyrTyrTyr 418
1818 GCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1867
418 snAlaThrPheGlnAsnLeuGlnLeuPheProGlyIleSerGlnValTyrHis 434
1868 ATGCACCTTTGACATCTGAGCCTTTTCCCGGCTGCGAAGTGTACAC 1917
435 SerSerGlnValGlyMetValPheGlyThrTyrProValAlaSerAlaThr 451

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|||||
1918 AGCTTGAAGTGGGATGGGCTTTTCTGATGTTGGCCAGAGTGGTAC 1967
451 FALDPEHGLHAGLHSTHSTSTYMEGLGALFPAALAP 498
1968 GCGCTTGGAGTGGTAAAGGAGAAATATGGAGGAGGCTGGGCGCT 2017
478 IGGALHYSASHTTMTASHTTHTGGLYTPYSGGLVALPHTASVAL 484
2018 TTGGTAAATATGATATATATGAGGCTGGGAGAACAGAGTGGTAAAGTGG 2067
485 ALALALDGLYSCTPROGLYSALAGLGLHVALASPVASPTROAL 501
2068 GATGGGCTTGGTTCACCAAGGCAACACCAATCCAGGCTTGGGCTTGGAC 2117
501 GHTHTASPTLHAGTYSALAGGLYTHFAGGLYTPHTHGLGAG 518
2118 GACCAATAGATTAATATGGAGCTTGGATATGGCTATATATATGAGTTGG 2167
518 THTHTTAAATATATATATATATATATATATATATATATATATATATAT 544
2168 GATATATGGGCTGGAGGAGCTTGGGAGGAGGAGGAGGAGGAGGAGGAG 2217
545 GYGLYSCTYSASPVASVALASPVVALVGLVGLVGLVGLVGLVGLVGLV 551
2218 GAGAGTAAATAGATTAATATATATATATATATATATATATATATATAT 2267
551 GSETGLYGLHGLHPTALATATATATATATATATATATATATATATATAT 568
2268 GAGGAGCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2317
568 GVALVGLHGLHGLHGLHGLHGLHGLHGLHGLHGLHGLHGLHGLHGLH 584
2318 TGGTCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2367
585 SETGLYPTROGLYATHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT 601
2468 TGGGCTGGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2417
601 GASPSTASHTTASHTTASHTTASHTTASHTTASHTTASHTTASHTTAS 618
2418 TGGAGAGTAAATATATATATATATATATATATATATATATATATAT 2467
618 TGGTCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 634
2468 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2517
635 GYPTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT 651
2518 GGTAAACCAATATATATATATATATATATATATATATATATATATAT 2567
651 ALASPTALALAGLGLHGLHGLHGLHGLHGLHGLHGLHGLHGLHGLH 668
2568 TGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2617
668 THTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT 684
2618 AGCATAGCTTCAATATATATATATATATATATATATATATATATATAT 2667
685 SGTVALSPTROALHGLHGLHGLHGLHGLHGLHGLHGLHGLHGLHGLH 701
2668 AGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2717
701 THTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT 718
2718 TGGGCTGGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2767
718 TGGTCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 734
2768 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2817
735 TGGTCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 751
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2818 CTGAGTAAATATATATATATATATATATATATATATATATATATAT 2867
751 SLVSTHGLYMEGLHSTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT 768
2868 CAAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2917
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2918 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2967
785 SETGLYPTROGLYATHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT 801
2968 TGGGCTGGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3017
801 SVALVGLHGLHGLHGLHGLHGLHGLHGLHGLHGLHGLHGLHGLH 818
3018 GGTGGTCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3067
818 TGGTCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 834
3068 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3117
835 TGTCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 851
3118 TGGTCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3167
851 NGLYPHTROGLYATHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT 868
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? Sequence ID, Application US/09352159A
? Patent No. 6211434
? GENERAL INFORMATION:
? APPLICANT: Duick, Jonathan P.
? APPLICANT: Gilliam, Jacob T.
? APPLICANT: Maddox, Joyce R.
? TITLE OF INVENTION: Amino Polypeptide Oxidase
? TITLE OF INVENTION: Polypeptides and Related Polypeptides and Methods of Use

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seq_date: 15-Aug-2002
patent_no: 6025188
GENERAL INFORMATION:
APPLICANT: DAVICK, Jonathan
INVENTOR: Madise, Joyce R.
APPLICANT: Wood, Tracy A.
TITLE OF INVENTION: FUMONISIN DETOXIFICATION COMPOSITIONS
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: Pioneer Hi-Bred International, 7100 N.W. 62nd Ave., P.O.
CITY: Johnston
STATE: Iowa
COUNTRY: USA
ZIP: 50131
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ACCESSION NUMBER: US-09-658-835c-25
FILING DATE: 07-JUL-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/484,815
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/289,595
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 42,734
ADDRESS: DAVICK, Jonathan
TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-888-949-15

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seq_documentation_block:
Sequence 15, Applicant: us-09-658-758
Patent No. 6238330
GENERAL INFORMATION:
APPLICANT: Davick, Jonathan
APPLICANT: Davick, Tracy E.
APPLICANT: Rood, Tracy A.
APPLICANT: Ward, Zia
TITLE OF INVENTION: PROMOTININ DETOXIFICATION COMPOSITIONS
NUMBER OF INVENTORS: 17
CORRESPONDENCE ADDRESS:
ADDRESS: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
CITY: Johnston
STATE: Iowa
COUNTRY: USA
ZIP: 50131
COMPUTER PROGRAM: P. 381.
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/262,758
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/484,815
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: us 08/289,595
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 272R3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1937 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-262-758-15

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BASE COUNT 207 a 215 c 250 g 224 t
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Percent Similarity:	64.773	Percent Identity:	40.909

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US-09-658-835C-25 x H100328

Align seq 1/1 to: B1100328 from: 1 to: 878

```

9 SerLeuPhleValValLeuLeuGly.....LeuSerAlaSerLeuAlaSe 24
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
24 ACCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 74
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
23 TGLYALPProthValValLeuLeuAlaValMetValValClyThrThr 40
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
74 TTGACCAACCTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 124
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
40 htrValValProGlyThrValAlaValValSerGluPhleLeuGlyValPro 56
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
124 TGAAGCAAAAGAGATTTTCACAGCGCTGGCGCTTTCCTGGAGATCGCG 174
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
52 htrAlaAlaSerPro.....ThrArgPhleAlaProProThrArgPro 70
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
174 TTGCTCAAAAGAGAGATTTTCACAGCGCTGGCGCTTTCCTGGAGATCG 224
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
76 oValProLysSerThrProLeuValAlaValThrAlaValProAlaLysP 87
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
224 AATGCTGCTGAGCTGAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 274
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
87 ProGluGluPhleAsnLysProGluGluGluArgGluGluGluThrMetAla 104
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
274 GGTCAAAAGAGAGATTTTCACAGCGCTGGCGCTTTCCTGGAGATCGCG 424
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
104 htrAsnLysProProSerAlaValCly.....SerGluAspLysLysAs 119
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
418 ...AAATGAAAGAGAGATTTTCACAGCGCTGGCGCTTTCCTGGAGAT 364
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
119 htrAsnLysLysValProGly.....ThrGluAsnLysLysLysAlaVal 144
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
465 GCTAAATATATTAACACCTGGAGATTTTCACAGCGCTGGCGCTTTCCT 414
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
144 dMetValThrLysProGlyValAlaValAlaValLysLysLysProPhe 156
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
415 TGAAGCAAAAGAGATTTTCACAGCGCTGGCGCTTTCCTGGAGATCGCG 464
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
151 htrLeuLysAspLysLysLysLysLysLysLysLysLysLysLysLys 167
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
462 ...AGCTTTGATGCAAGGCTCTCTCTCAATGAAATGCTGCTGCTGCT 508
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
167 LThrLysAsnValAlaThrAsnLysLeuLysLysLysLysLysLysLysL 184
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
509 GGCATGCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 557
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
184 GUPProLysThrGluValAsnLysLysLysLysLysLysLysLysLysL 200

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558 .....|::|::|::|::|::|::|::|::|::|::|::|::|
558 ...GAACACAGCTGAGGAGAACTGGGCTCATTTGGACCAATGGCTGCTGG 605
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
201 ASPTFFVALGILATGASnLysLysLysLysLysLysLysLysLysLys 217
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
605 CAAGGCTGAGGAGCAATATGGTAACTTTGGGAGGAGAGAGAGAGAGAG 654
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
217 LThrLysGlyLysLysLysLysLysLysLysLysLysLysLysLysL 224
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
655 GATGATCTTTCATATGATGATGATGATGATGATGATGATGATGATGAT 704
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
234 htrMetProLysLysLysLysLysLysLysLysLysLysLysLysL 250
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
705 TGTGCCCCATTTGTGCAAGAGAGCTCTTCACAGAGGAGATTTCTGACAG 754
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
250 GVALAlaAsnLysLysLysLysLysLysLysLysLysLysLysLysL 263
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
755 TGTG.....GGCTTTCATTTGGAGAAATGTTACCAAA 785

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